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PATENT

Please amend the specification in adherence with 37 C.F.R. § 1.821-1.825 as follows:

<u>IN THE SPECIFICATION:</u>

Please replace the paragraph beginning on page 6, line12, with the following amended paragraph:

Figure 4. Amino acid sequences of the light chain (A) (SEQ ID NOS:1-2) and the heavy chain (B) (SEQ ID NOS:3-4) variable regions of the humanized 1D10 antibody (upper lines) and mouse 1D10 antibody (lower lines), not including the signal sequences. The three CDRs in each chain are underlined. Residues in the human framework that have been replaced with mouse amino acids or consensus human amino acids are doubly underlined. Amino acid sequences of the complete light chain and the heavy chain of the humanized 1D10 are shown in (C)(SEQ ID NO:5) and (E) (SEQ ID NO:7), respectively. The V_L domain consists of residues 1-107, and the C_K 108-214. The V_H domain consists of residues 1-116, the C_H1 117-214, the hinge 215-229, the C_H2 230-339, and the C_H3 domain 340-446. Amino acid sequence of the Fd-Jun in the humanized F(ab'-zipper)$_2$ of 1D10 is shown in (D) (SEQ ID NO:6). The V_H domain consists of residues 1-116, the C_H1 domain 117-214, the modified hinge 215-234, and the Fos leucine zipper 235-273.

Please replace the paragraph beginning on page 6, line 28, with the following replacement paragraph:

Figure 5. Amino acid sequence of the light chain (A) (SEQ ID NOS:8-9) and the heavy chain (B) (SEQ ID NOS:10-11) variable regions of the humanized M291 antibody (upper lines) and the mouse M291 antibody (lower lines), not including the signal sequences. The three CDRs in each chain are underlined. Residues in the human framework that have been replaced with mouse amino acids or consensus human amino acids are doubly underlined. Amino acid sequences of the complete light chain of the humanized M291 are shown in (C) (SEQ ID NO:12). The V_L domain consists of residues 1-106, and the human C_K domain 107-213. Amino acid sequence of the Fd-Fos in the humanized F(ab'zipper)2 of M291 is shown in D (SEQ ID NO:13). The V_H domain